

-1-

SEQUENCE LISTING

<110> Vertino, Paula M.

<120> TMS1 Compositions and Methods of Use

<130> E0355/7003/ERG/MAT

<150> US 60/159,975

<151> 1999-10-18

<160> 27

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2821

<212> DNA

<213> Homo Sapiens

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ccacacacag ctatccag gtacattttt gacgcttagga attcagcaaa gaataagaca	300
gttaaggctt ccgatgctca taggcctcac attttagaga gggatgaatg tccaataagc	360
atataaaacat ataatatgtc agggtcgat gactacaagg aacagtgatt gttacaaccc	420
agatgagagg gaaaaataaa ggattccaaa tatccccctt gggaaatgaga gtcaggattc	480
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ccaggcctgc actttataga ccagcaccgg gctgcgttca tcgcgagggt cacaaacgtt	2160
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aaaagaggca tgtacccaaag ggcgcaaact ggtggcagc tctgtccaag ccatttagaa 2760
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a 2821

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<213> Homo Sapiens

<220>
<221> CDS
<222> (75) ... (662)

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Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu
1 5 10

gag aac ctg acc gcc gag ctc aag aag ttc aag ctg aag ctg ctg 158
Glu Asn Leu Thr Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu
15 20 25

tgc gtg ccg ctg cgc gag ggc tac ggg cgc atc ccg cgg ggc gcg ctg 206
Ser Val Pro Leu Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu
30 35 40

ctg tcc atg gac gcc ttg gac ctc acc gac aag ctg gtc agc ttc tac 254
Leu Ser Met Asp Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr
45 50 55 60

ctg gag acc tac ggc gcc gag ctc acc gct aac gtg ctg cgc gac atg 302
Leu Glu Thr Tyr Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met
65 70 75

ggc ctg cag gag atg gcc ggg cag ctg cag gcg gcc acg cac cag ggc 350
Gly Leu Gln Glu Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly
80 85 90

tct gga gcc gcg cca gct ggg atc cag gcc cct cct cag tcg gca gcc 398
Ser Gly Ala Ala Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala
95 100 105

aag cca ggc ctg cac ttt ata gac cag cac cgg gct gcg ctt atc gcg 446
Lys Pro Gly Leu His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala
110 115 120

agg gtc aca aac gtt gag tgg ctg ctg gat gct ctg tac ggg aag gtc 494
Arg Val Thr Asn Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val
125 130 135 140

ctg acg gat gag cag tac cag gca gtg cgg gcc gag ccc acc aac cca 542

Leu Thr Asp Glu Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro
145 150 155

agc aag atg cgg aag ctc ttc agt ttc aca cca gcc tgg aac tgg acc 590
Ser Lys Met Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr
160 165 170

tgc aag gac ttg ctc ctc cag gcc cta agg gag tcc cag tcc tac ctg 638
Cys Lys Asp Leu Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu
175 180 185

gtg gag gac ctg gag cgg agc tga ggctccttcc cagcaacact ccggtagcc 692
Val Glu Asp Leu Glu Arg Ser *
190 195

cctggcaatc ccaccaaatac atcctgaatc tgatctttt atacacaata tacgaaaagc 752
cagcttgaaa aaaaaaaaaa 770

<210> 3
<211> 195
<212> PRT
<213> Homo Sapiens

<400> 3

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Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser Met Asp
35 40 45
Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr
50 55 60
Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu
65 70 75 80
Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly Ser Gly Ala Ala
85 90 95
Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala Lys Pro Gly Leu
100 105 110
His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr Asn
115 120 125
Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp Glu
130 135 140
Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met Arg
145 150 155 160
Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp Leu
165 170 175
Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp Leu
180 185 190

Glu Arg Ser
195

<210> 4
<211> 626
<212> DNA
<213> Homo Sapiens

<400> 4

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aaggcgggga gtccaggttc cgccccggag ccgacttctt cctggtcggc ggctgcagcg
gggtgagcgg cggcagcggc cgggatcct ggagccatgg ggcgcgcgcg cgacgccatc 120
180

ctggatgcgc tggagaacct gaccggcag gagctaaga agttcaagct gaagctgctg 240
tcggtgccgc tgcgcgaggc ctacgggcgc atcccgcggg gcgcgctgct gtccatggac 300
gccttggacc tcaccgacaa gctggtcagc ttctacctgg agacctacgg cgccgagctc 360
accctaactg tgctgcgcga catgggcctg caggagatgg ccgggcagct gcaggcgccc 420
acgcaccagg gtgagccgccc cccgttcccc tccacccctt ctttccctc cacccacacc 480
agcgttacc ccgcgggctc ttccgtttc tgttcctctt acccctaaac aaagctgtc 540
tacccgaaag gaggctcccc acgcttggcc taccgaccaa cgggaccccg gccccacggc 600
gggaagggaa gggaaagggaa tcactt 626

<210> 5
<211> 339
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> (67)...(339)

<400> 5

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ggagcc atg ggg cgc gcg gac gcc atc ctg gat gcg ctg gag aac 108
Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn
1 5 10

ctg acc gcc gag gag ctc aag aag ttc aag ctg aag ctg ctg tcg gtg 156
Leu Thr Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val
15 20 25 30

ccg ctg cgc gag ggc tac ggg cgc atc ccg cgg ggc gcg ctg ctg tcc 204
Pro Leu Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser
35 40 45

atg gac gcc ttg gac ctc acc gac aag ctg gtc agc ttc tac ctg gag 252
Met Asp Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu
50 55 60

acc tac ggc gcc gag ctc acc gct aac gtg ctg cgc gac atg ggc ctg 300
Thr Tyr Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu
65 70 75

cag gag atg gcc ggg cag ctg cag gcg gcc acg cac cag g 340
Gln Glu Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln
80 85 90

<210> 6
<211> 91
<212> PRT
<213> Homo Sapiens

<400> 6

Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr 15
1 5 10 15
Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu Ser Val Pro Leu 30
20 25 30
Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Ser Met Asp 45
35 40 45
Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr 60
50 55 60
Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met Gly Leu Gln Glu

gac ttg ctc ctc cag gcc cta agg gag tcc cag tcc tac ctg gtg gag 239
Asp Leu Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu
65 70 75

gac ctg gag cg^g agc tga g gctc^cttccc agcaacactc cggtcagccc 288
Asp Leu Glu Arg Ser *
80

ctggcaatcc caccaa^aatca tcctgaatct gatctttta tacacaat^aat acgaaaagcc 348 .
agcttgaa 356

<210> 10
<211> 84
<212> PRT
<213> Homo Sapiens

<400> 10
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5 10 15
Asn Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp 20
25 30
Glu Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met 35
40 45
Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp 50
55 60
Leu Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp 65
70 75 80
Leu Glu Arg Ser

<210> 11
<211> 18
<212> DNA
<213> Homo Sapiens

<400> 11
gcacttata gaccagca 18

<210> 12
<211> 18
<212> DNA
<213> Homo Sapiens

<400> 12
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<210> 13
<211> 17
<212> DNA
<213> Homo Sapiens

<400> 13
tgggcctgca ggagatg 17

<210> 14
<211> 22
<212> DNA
<213> Homo Sapiens

<400> 14

ccttcctggg catggagtcc tg	22
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<400> 17 caaaacatcc ataaacaaca acaca	25
<210> 18 <211> 19 <212> DNA <213> Homo Sapiens	
<400> 18 tttagcgccc gttagcggc	19
<210> 19 <211> 22 <212> DNA <213> Homo Sapiens	
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<210> 20 <211> 803 <212> DNA <213> Mus Musculus	
<220> <221> CDS <222> (162)...(743)	
<400> 20 ggaaaagaac aggagctgta agaaaaaggagg gtgggggagt cccagcatgc ccatcggcct aagcagctga ctccctggtc ttggcggct ggcagcaggc aggctgagca ggcgagcagc	60 120

agcaagagta aaagggtgacc gcggctgccc accccagagc c atg ggg cg gca cga 176
Met Gly Arg Ala Arg
1 5

gat gcc atc ctg gac gct ctt gaa aac ttg tca ggg gat gaa ctc aaa 224
Asp Ala Ile Leu Asp Ala Leu Glu Asn Leu Ser Gly Asp Glu Leu Lys
10 15 20

aag ttc aag atg aag ctg ctg aca gtg caa ctg cga gaa ggc tat ggg 272
Lys Phe Lys Met Lys Leu Leu Thr Val Gln Leu Arg Glu Gly Tyr Gly
25 30 35

cgc atc cca cgc ggg gcc ctg ctg cag atg gac gcc ata gat ctc act 320
Arg Ile Pro Arg Gly Ala Leu Leu Gln Met Asp Ala Ile Asp Leu Thr
40 45 50

gac aaa ctt gtc agc tac tat ctg gag tcg tat ggc ttg gag ctc aca 368
Asp Lys Leu Val Ser Tyr Tyr Leu Glu Ser Tyr Gly Leu Glu Leu Thr
55 60 65

atg act gtg ctt aga gac atg ggc tta cag gag ctg gct gag cag ctg 416
Met Thr Val Leu Arg Asp Met Gly Leu Gln Glu Leu Ala Glu Gln Leu
70 75 80 85

caa acg act aaa gaa gag tct gga gct gtg gca gct gca gcc agt gtc 464
Gln Thr Thr Lys Glu Ser Gly Ala Val Ala Ala Ala Ser Val
90 95 100

cct gct cag agt aca gcc aga aca gga cac ttt gtg gac cag cac agg 512
Pro Ala Gln Ser Thr Ala Arg Thr Gly His Phe Val Asp Gln His Arg
105 110 115

caa gca ctc att gcc agg gtc aca gaa gtg gac gga gtg ctg gat gct 560
Gln Ala Leu Ile Ala Arg Val Thr Glu Val Asp Gly Val Leu Asp Ala
120 125 130

ttg cat ggc agt gtg ctg act gaa gga cag tac cag gca gtt cgt gca 608
Leu His Gly Ser Val Leu Thr Glu Gly Gln Tyr Gln Ala Val Arg Ala
135 140 145

gag acc acc agc caa gac aag atg agg aag ctc ttc agc ttt gtt cca 656
Glu Thr Thr Ser Gln Asp Lys Met Arg Lys Leu Phe Ser Phe Val Pro
150 155 160 165

tcc tgg aac ctg acc tgc aag gac tcc ctc ctc cag gcc ttg aag gaa 704
Ser Trp Asn Leu Thr Cys Lys Asp Ser Leu Leu Gln Ala Leu Lys Glu
170 175 180

ata cat ccc tac ttg gtg atg gac ctg gag cag agc tga ggtatcttt 753
Ile His Pro Tyr Leu Val Met Asp Leu Glu Gln Ser *
185 190

ccagctacat tatcttagctc ctgactttgt atacacaatt tttaaaaaaa 803

<210> 21
<211> 193
<212> PRT
<213> Mus Musculus

<400> 21

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Gly Asp Glu Leu Lys Lys Phe Lys Met Lys Leu Leu Thr Val Gln Leu
20 25 30
Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu Leu Gln Met Asp
35 40 45
Ala Ile Asp Leu Thr Asp Lys Leu Val Ser Tyr Tyr Leu Glu Ser Tyr
50 55 60
Gly Leu Glu Leu Thr Met Thr Val Leu Arg Asp Met Gly Leu Gln Glu
65 70 75 80
Leu Ala Glu Gln Leu Gln Thr Thr Lys Glu Glu Ser Gly Ala Val Ala
85 90 95
Ala Ala Ala Ser Val Pro Ala Gln Ser Thr Ala Arg Thr Gly His Phe
100 105 110
Val Asp Gln His Arg Gln Ala Leu Ile Ala Arg Val Thr Glu Val Asp
115 120 125
Gly Val Leu Asp Ala Leu His Gly Ser Val Leu Thr Glu Gly Gln Tyr
130 135 140
Gln Ala Val Arg Ala Glu Thr Thr Ser Gln Asp Lys Met Arg Lys Leu
145 150 155 160
Phe Ser Phe Val Pro Ser Trp Asn Leu Thr Cys Lys Asp Ser Leu Leu
165 170 175
Gln Ala Leu Lys Glu Ile His Pro Tyr Leu Val Met Asp Leu Glu Gln
180 185 190
Ser

<210> 22
<211> 605
<212> DNA
<213> Rattus Norvegicus

<220>
<221> CDS
<222> (2)...(518)

<400> 22

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Phe Lys Ile Lys Leu Leu Thr Ala Pro Val Arg Glu Gly Tyr Gly Arg
1 5 10 15

atc cca cgg ggg gcc ctg ctg cag atg gac ccc ata gac ctc act gat 97
Ile Pro Arg Gly Ala Leu Leu Gln Met Asp Pro Ile Asp Leu Thr Asp
20 25 30

aaa ctc gtc agy tac tat ctg gag ggg tat ggc ttg gag ctc aca atg 145
Lys Leu Val Xaa Tyr Tyr Leu Glu Gly Tyr Gly Leu Glu Leu Thr Met
35 40 45

act gtg ctt aga gac atg ggc ata cag gag ctg gct gag cag ctg caa 193
Thr Val Leu Arg Asp Met Gly Ile Gln Glu Leu Ala Glu Gln Leu Gln
50 55 60

aag att atg gaa gag tct gga gct gtg gct act gca acc agt gtc cct 241
Lys Ile Met Glu Glu Ser Gly Ala Val Ala Thr Ala Thr Ser Val Pro
65 70 75 80

gct cag ggc aca gcc aga aca gaa cat ttt gtg gac caa cac agg caa 289
Ala Gln Gly Thr Ala Arg Thr Glu His Phe Val Asp Gln His Arg Gln
85 90 95

gca ctc att gcc agg gtc aca gaa gtt gat ggt ttg ctg gat gct ctg
 Ala Leu Ile Ala Arg Val Thr Glu Val Asp Gly Leu Leu Asp Ala Leu
 100 105 110
 337

tat ggc aat gtg ctg act gaa gga cag tac cag gca gtt cgt gca gag
 Tyr Gly Asn Val Leu Thr Glu Gly Gln Tyr Gln Ala Val Arg Ala Glu
 115 120 125
 385

acc acc aac caa aac aag atg agg aag ctc ttt agc ttt gct cca gcc
 Thr Thr Asn Gln Asn Lys Met Arg Lys Leu Phe Ser Phe Ala Pro Ala
 130 135 140
 433

tgg aac ctg acc tgc aag aac ttg ttc ctt gag gcc ttg agg caa aca
 Trp Asn Leu Thr Cys Lys Asn Leu Phe Leu Glu Ala Leu Arg Gln Thr
 145 150 155 160
 481

cag ccc tac ttg gtg aca gac ctg gaa cag agc tga g gtatctttc
 Gln Pro Tyr Leu Val Thr Asp Leu Glu Gln Ser *
 165 170
 528

cagctacaca tctagctcct ggttttgtat acaaaaatttt ctaaaaaacaa gtttgtattt
 gtgttttctc gaaaaaaaa
 588
 605

<210> 23
 <211> 171
 <212> PRT
 <213> Rattus Norvegicus

<400> 23
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 1 5 10 15
 Ile Pro Arg Gly Ala Leu Leu Gln Met Asp Pro Ile Asp Leu Thr Asp
 20 25 30
 Lys Leu Val Xaa Tyr Tyr Leu Glu Gly Tyr Gly Leu Glu Leu Thr Met
 35 40 45
 Thr Val Leu Arg Asp Met Gly Ile Gln Glu Leu Ala Glu Gln Leu Gln
 50 55 60
 Lys Ile Met Glu Glu Ser Gly Ala Val Ala Thr Ala Thr Ser Val Pro
 65 70 75 80
 Ala Gln Gly Thr Ala Arg Thr Glu His Phe Val Asp Gln His Arg Gln
 85 90 95
 Ala Leu Ile Ala Arg Val Thr Glu Val Asp Gly Leu Leu Asp Ala Leu
 100 105 110
 Tyr Gly Asn Val Leu Thr Glu Gly Gln Tyr Gln Ala Val Arg Ala Glu
 115 120 125
 Thr Thr Asn Gln Asn Lys Met Arg Lys Leu Phe Ser Phe Ala Pro Ala
 130 135 140
 Trp Asn Leu Thr Cys Lys Asn Leu Phe Leu Glu Ala Leu Arg Gln Thr
 145 150 155 160
 Gln Pro Tyr Leu Val Thr Asp Leu Glu Gln Ser
 165 170
 528

<210> 24
 <211> 713
 <212> DNA
 <213> Homo Sapiens

<220>
 <221> CDS

<222> (75) ... (605)

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gggatccctgg agcc atg ggg cgc gcg cgc gac gcc atc ctg gat gcg ctg 110
Met Gly Arg Ala Arg Asp Ala Ile Leu Asp Ala Leu
1 5 10

gag aac ctg acc gcc gag gag ctc aag aag ttc aag ctg aag ctg ctg 158
Glu Asn Leu Thr Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu
15 20 25

tcg gtg ccg ctg cgc gag ggc tac ggg cgc atc ccg cgg ggc gcg ctg 206
Ser Val Pro Leu Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu
30 35 40

ctg tcc atg gac gcc ttg gac ctc acc gac aag ctg gtc agc ttc tac 254
Leu Ser Met Asp Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr
45 50 55 60

ctg gag acc tac ggc gcc gag ctc acc gct aac gtg ctg cgc gac atg 302
Leu Glu Thr Tyr Gly Ala Glu Leu Thr Ala Asn Val Leu Arg Asp Met
65 70 75

ggc ctg cag gag atg gcc ggg cag ctg cag gcg gcc acg cac cag ggc 350
Gly Leu Gln Glu Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly
80 85 90

ctg cac ttt ata gac cag cac cgg gct gcg ctt atc gcg agg gtc aca 398
Leu His Phe Ile Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr
95 100 105

aac gtt gag tgg ctg ctg gat gct ctg tac ggg aag gtc ctg acg gat 446
Asn Val Glu Trp Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp
110 115 120

gag cag tac cag gca gtg cgg gcc gag ccc acc aac cca agc aag atg 494
Glu Gln Tyr Gln Ala Val Arg Ala Glu Pro Thr Asn Pro Ser Lys Met
125 130 135 140

cgg aag ctc ttc agt ttc aca cca gcc tgg aac tgg acc tgc aag gac 542
Arg Lys Leu Phe Ser Phe Thr Pro Ala Trp Asn Trp Thr Cys Lys Asp
145 150 155

ttg ctc ctc cag gcc cta agg gag tcc cag tcc tac ctg gtg gag gac 590
Leu Leu Leu Gln Ala Leu Arg Glu Ser Gln Ser Tyr Leu Val Glu Asp
160 165 170

ctg gag cgg agc tga ggctccttcc cagcaacact ccggcagcc cctggcaatc 645
Leu Glu Arg Ser *
175

ccaccaaatac atcctgaatc tgatctttt atacacaata tacgaaaagc cagttgaaa 705
aaaaaaaaa 713

<210> 25
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Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly Leu His Phe Ile
85 90 95
Asp Gln His Arg Ala Ala Leu Ile Ala Arg Val Thr Asn Val Glu Trp
100 105 110
Leu Leu Asp Ala Leu Tyr Gly Lys Val Leu Thr Asp Glu Gln Tyr Gln
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130 135 140
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Glu Asn Leu Thr Ala Glu Glu Leu Lys Lys Phe Lys Leu Lys Leu Leu
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Ser Val Pro Leu Arg Glu Gly Tyr Gly Arg Ile Pro Arg Gly Ala Leu
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ctg tcc atg gac gcc ttg gac ctc acc gac aag ctg gtc agc ttc tac 254
Leu Ser Met Asp Ala Leu Asp Leu Thr Asp Lys Leu Val Ser Phe Tyr
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ctg gag acc tac ggc gcc gag ctc acc gct aac gtg ctg cgc gac atg 302
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Gly Leu Gln Glu Met Ala Gly Gln Leu Gln Ala Ala Thr His Gln Gly
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Pro Ala Gly Ile Gln Ala Pro Pro Gln Ser Ala Ala Lys Pro
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